

Figure 1:

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AS 01: 3'-teg-G*G*G C*C*C*G G*C A*C*C G*T*C*C T*T*C*G
AS 02: 3'-teg-G*G*G*T*C A A G*C*C*C T*C*T G*T A*C*C*G
AS 03: 3'-teg-G*C*C*C T*C*T G*T A*C*C G*C*C*C G*C*A*A
AS 04: 3'-teg-T*A*C*C G*C*C*C G*C A A*T*T*T*C G A*G*A
AS 05: 3'-teg-T*T*C*G A G A*G*C A*C*C G*T A A*T A*G*G
AS 06: 3'-teg-G*A*A*T A*C G A*C*C*C*T A*C A*C G G*A*A
AS 07: 3'-teg-A*C*A*C G G A A*T*C*T C*C*T*A A*T A*C*C
AS 08: 3'-teg-C*T*C*C*T A A*T A*C*C G*C A A*A*T G*A*C
AS 09: 3'-teg-C*C*G*C*A A A*T G A*C*C*G G G A*A T*A*A
AS 10: 3'-teg-A*C*G G A*C A G*C*C*C T*T*G A*C*C G*T*A
AS 11: 3'-teg-G*G*A*C A G*C*C*C T*T*G A*C*C G*T A*T A*A*A
AS 12: 3'-teg-G*C*C*C T*T*G A*C*C G*T A*T A A*A G*A*A
AS 13: 3'-teg-G*G*A A*C*A*C A A*C*C*G T*C*C*G T*T*A*C
AS 14: 3'-teg-T*G*T A*C A*C G*T G*T A*C G*C*C G*T A*A
AS 15: 3'-teg-G*C*C*T C*C*T G*T C*C*A G*C*C*G C*C*A*A
AS 16: 3'-teg-G*G*A*C*C G A*C*A T*T*G C*A*C G*T C*T A*A*A

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\*: Thioester

\_: 2'-O-Methylation

teg: Triethylene glycol spacer

Figure 2

|                | 10     | 20   | 30 | 40 | 50 | 60 |
|----------------|--------|--|----|----|----|----|
| OB-RGRP_human  | -----  | MAG-VKALVALSFSGAIGLTFLMLGCALEDYGVYWPLFVLIFHAIS         |    |    |    |    |
| My47_human     | -----  | MAG- IKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILS        |    |    |    |    |
| yt02_C.elegans | MCCHIH | IQCFDCCSMKNTILAVAALAFAGVVGLTFLVLGCALPRYGTWTPMFVITFYVLS |    |    |    |    |
| YJ14_Yeast     | -----  | MMEFKVSP LTKIISLSGFLALGFLLVILSCAL--FHNYYPLFDILIFLLA    |    |    |    |    |
| Consensus      | MCCHIH | IQCF2222MAG2IKALI2LSF4GAIGLTFLMLGCALP3YG4YWPLFV24FY4LS |    |    |    |    |

|                | 70     | 80  | 90   | 100 | 110 | 120 |
|----------------|--------|---|--|-----|-----|-----|
| OB-RGRP_human  | PIPHFI | AKR----   | VTYDSDATSSACRELAYFFTTGIVVSAFGFPVILARVAVIKWGACG |     |     |     |
| My47_human     | PIPYCI | ARR----   | LVDDTDAMSNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACA |     |     |     |
| yt02_C.elegans | PVPLLI | ARR----   | FQEDMTGTN-ACIELALFITTGIVISAFALPIVLAHAGTIAMSACF |     |     |     |
| YJ14_Yeast     | PIPNTI | FNAGNKYHTSDFMSDSSNTGQDLAHFLTGLMLVTSGIALPVVFYHCQLIGHLSCI |  |     |     |     |
| Consensus      | PIP44I | ARRGNKYH44DDMDATSNAC4ELA4FLTGTGIVVSAF2LP2V2A2A4LI4WGAC4 |  |     |     |     |

|                | 130              | 140                          | 150 |
|----------------|------------------|------------------------------|-----|
| OB-RGRP_human  | LVLAGNAVIFLTIQGF | FLIFGRGDDFSWEQW-             |     |
| My47_human     | LVLTGNTVIFATILG  | FFLVFGSKDDFSWQQW-            |     |
| yt02_C.elegans | LIFIANSENFSVIIF  | YFRIFNGEDMNGMSLW-            |     |
| YJ14_Yeast     | MCMIGGLIIYSSIVIF | KWFFKKDFENEDDSLFG            |     |
| Consensus      | LVLI             | GN42IFSTI4GFFLIFG44DDFSWS2WG |     |

Figure 3A

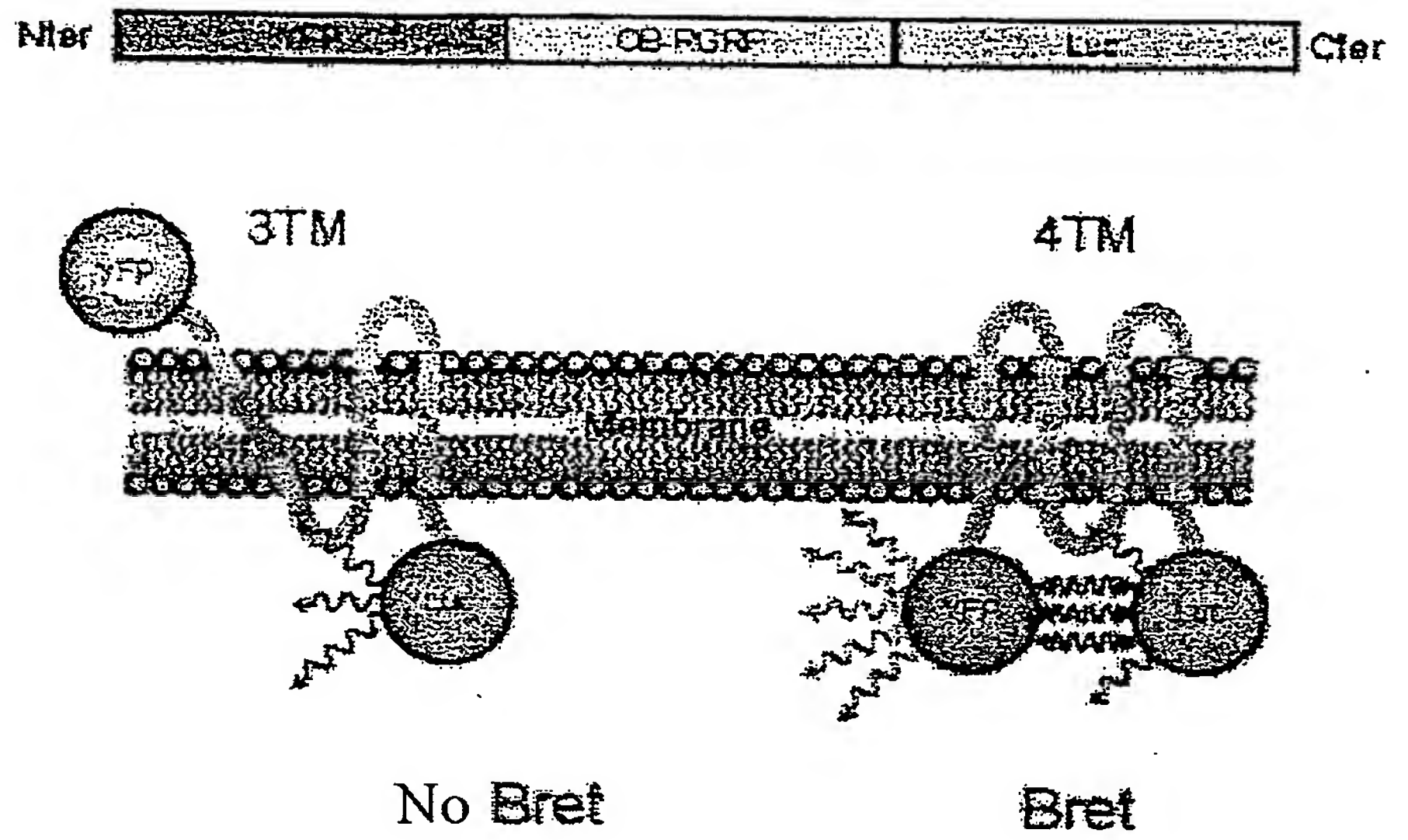


Figure 3B

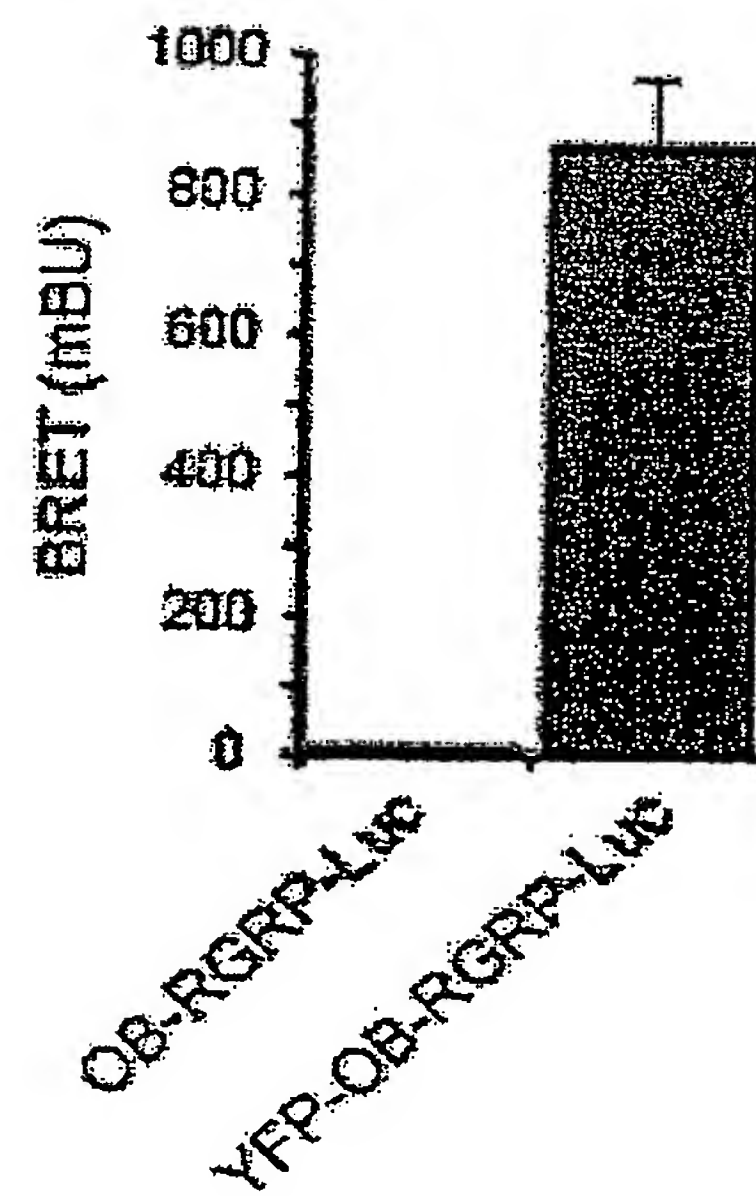


Figure 4 A

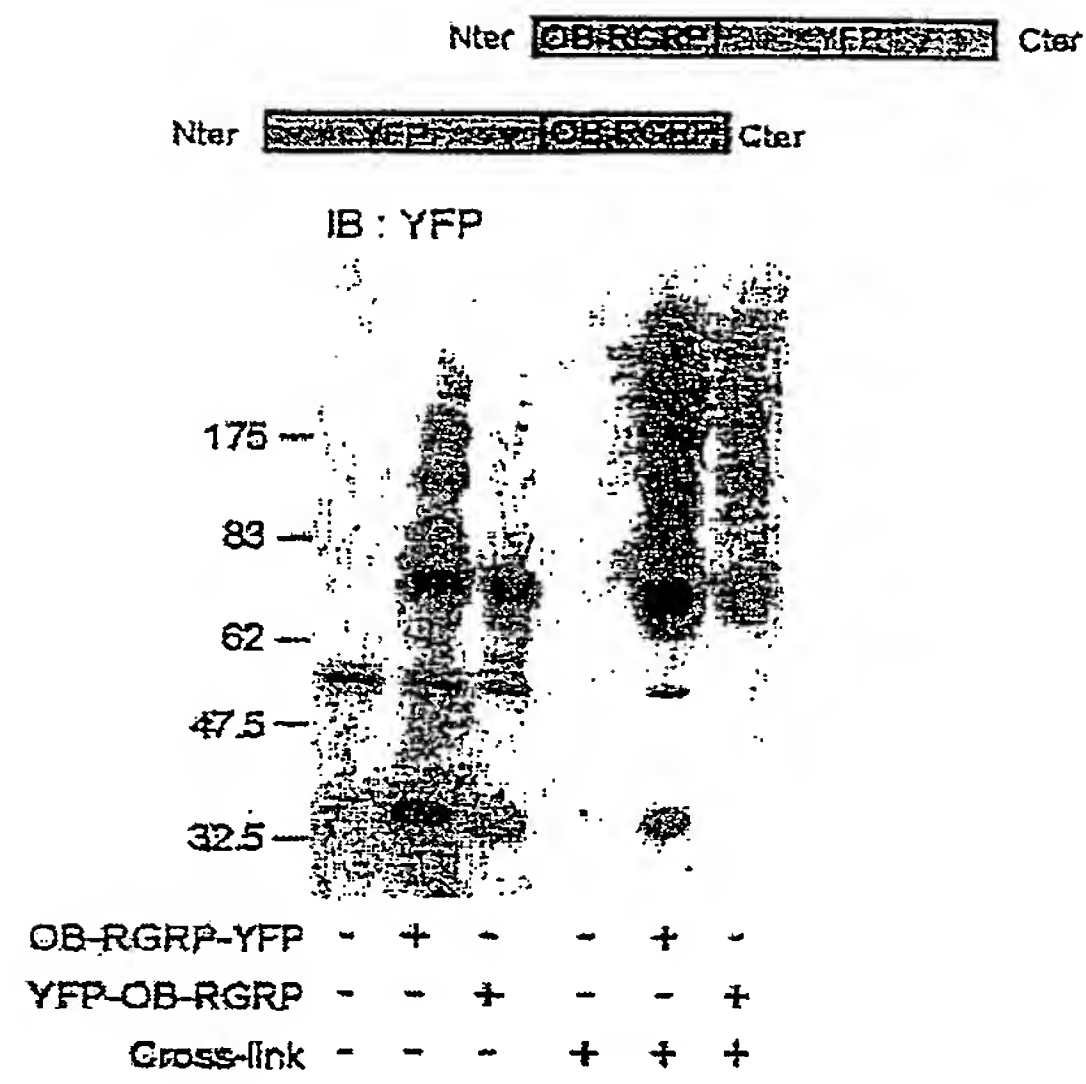
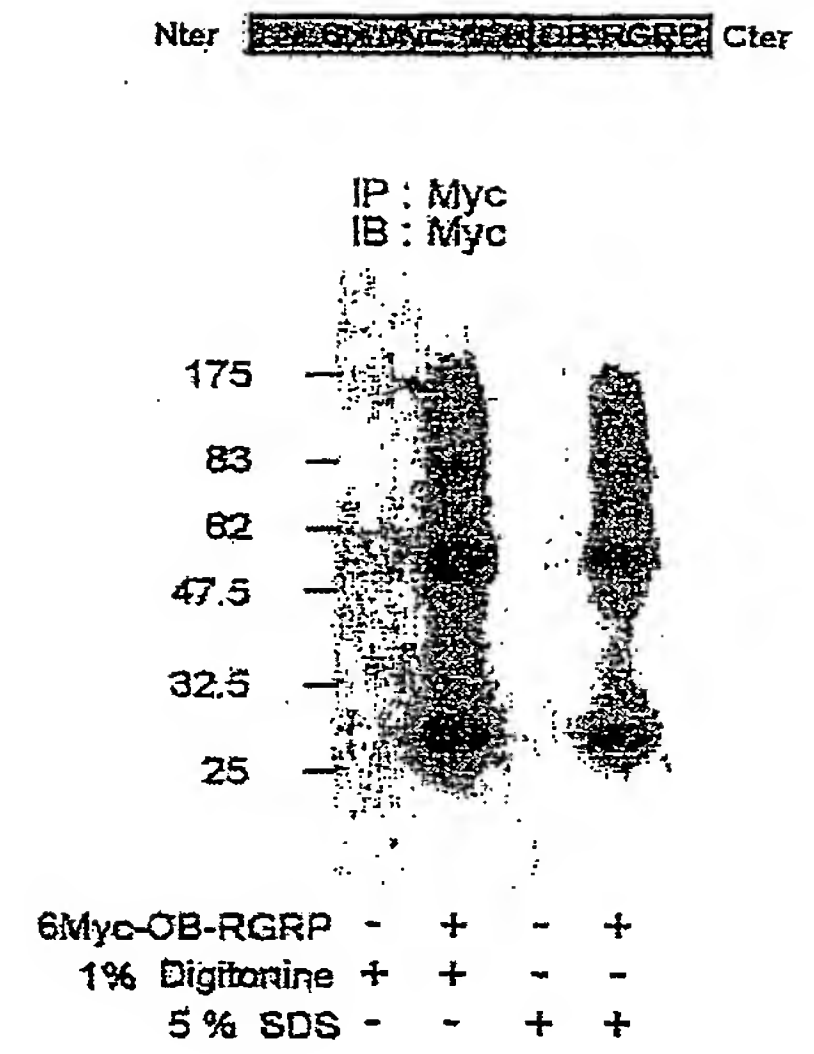


Figure 4B



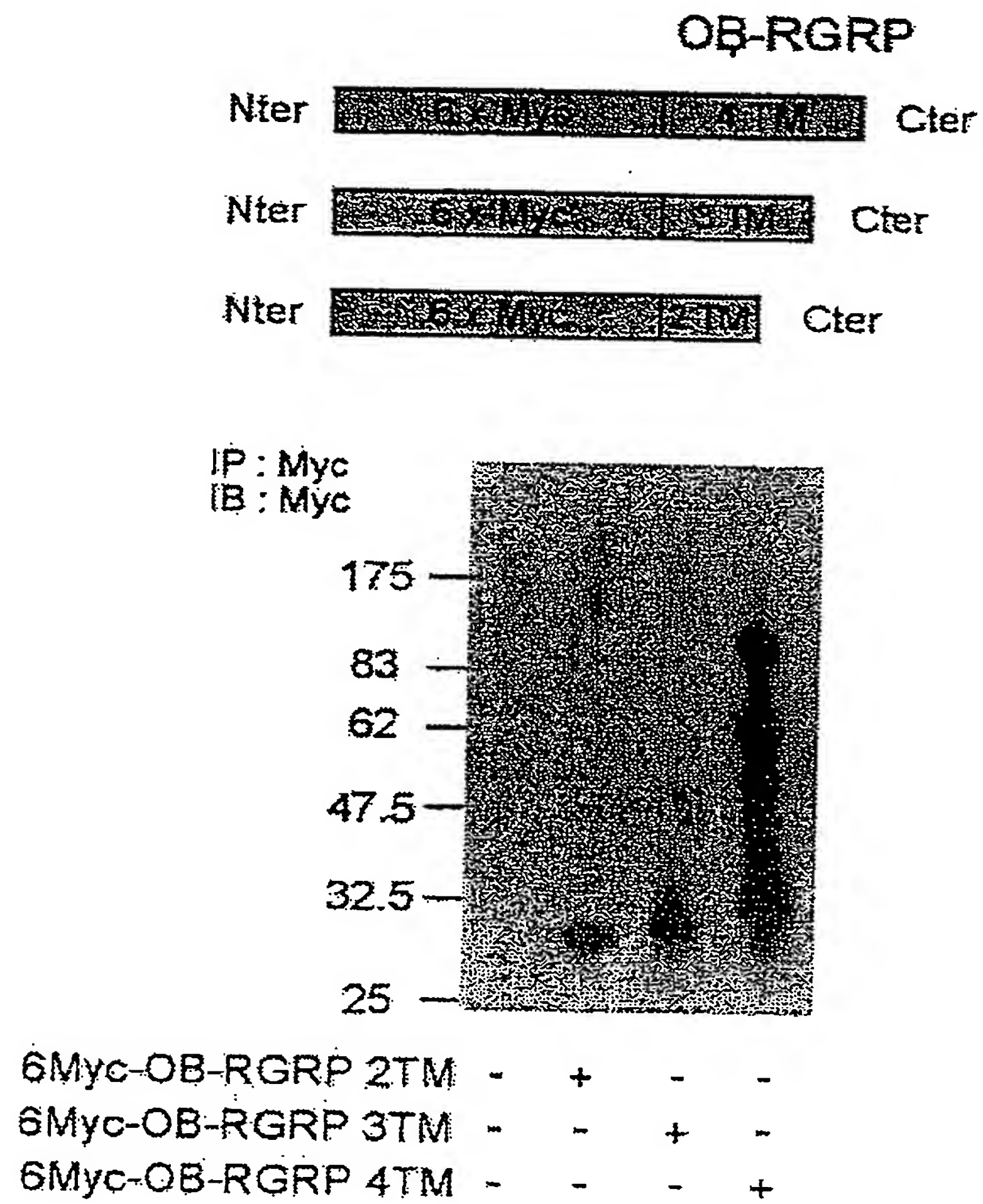
**Figure 5**

Figure 6 A

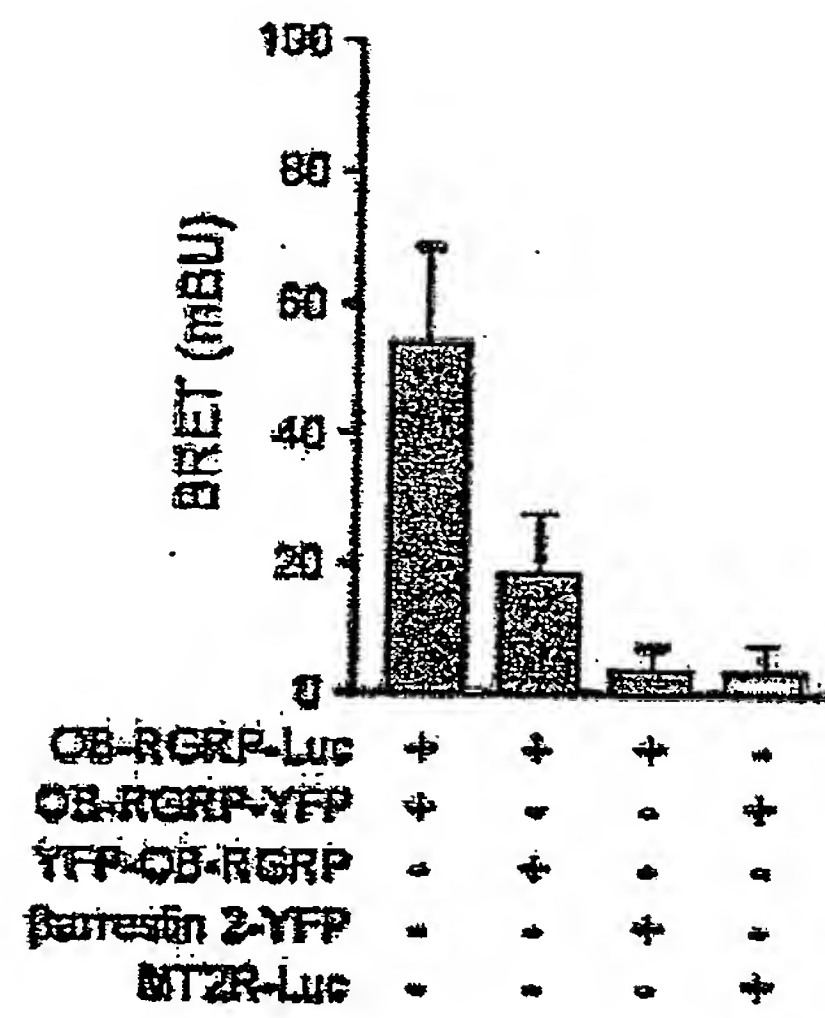
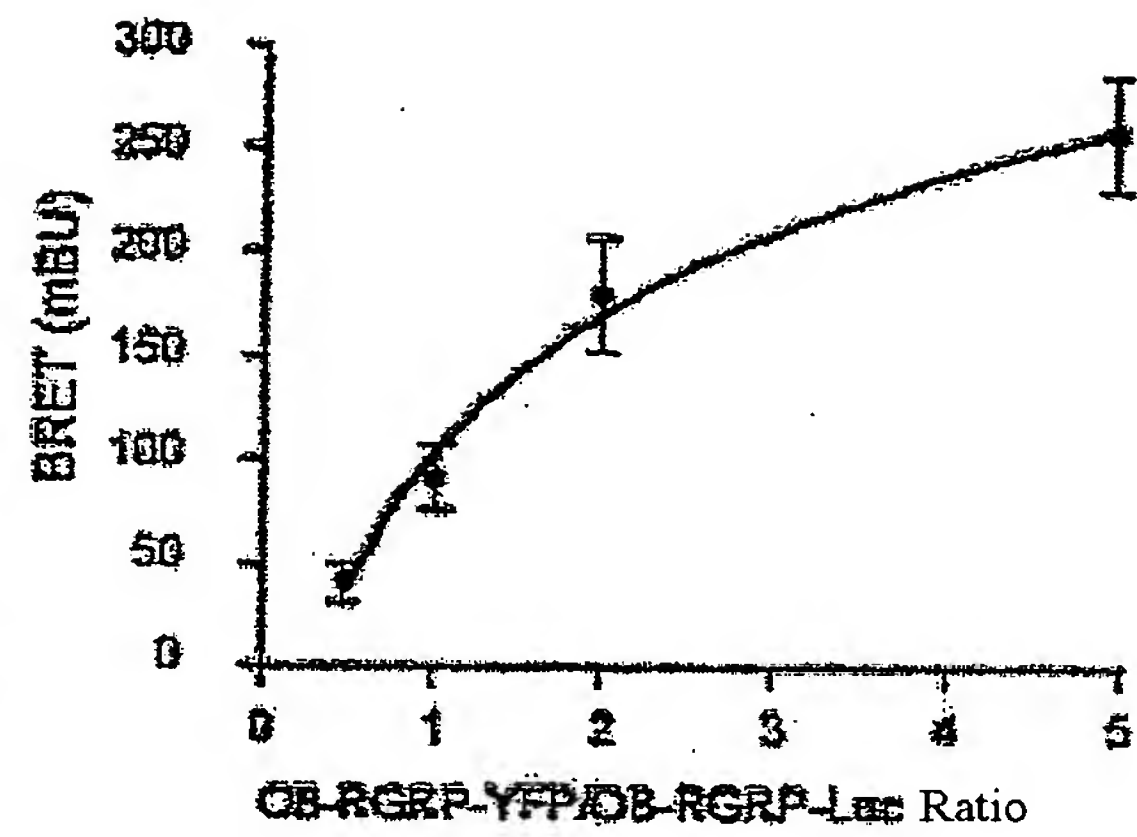


Figure 6B



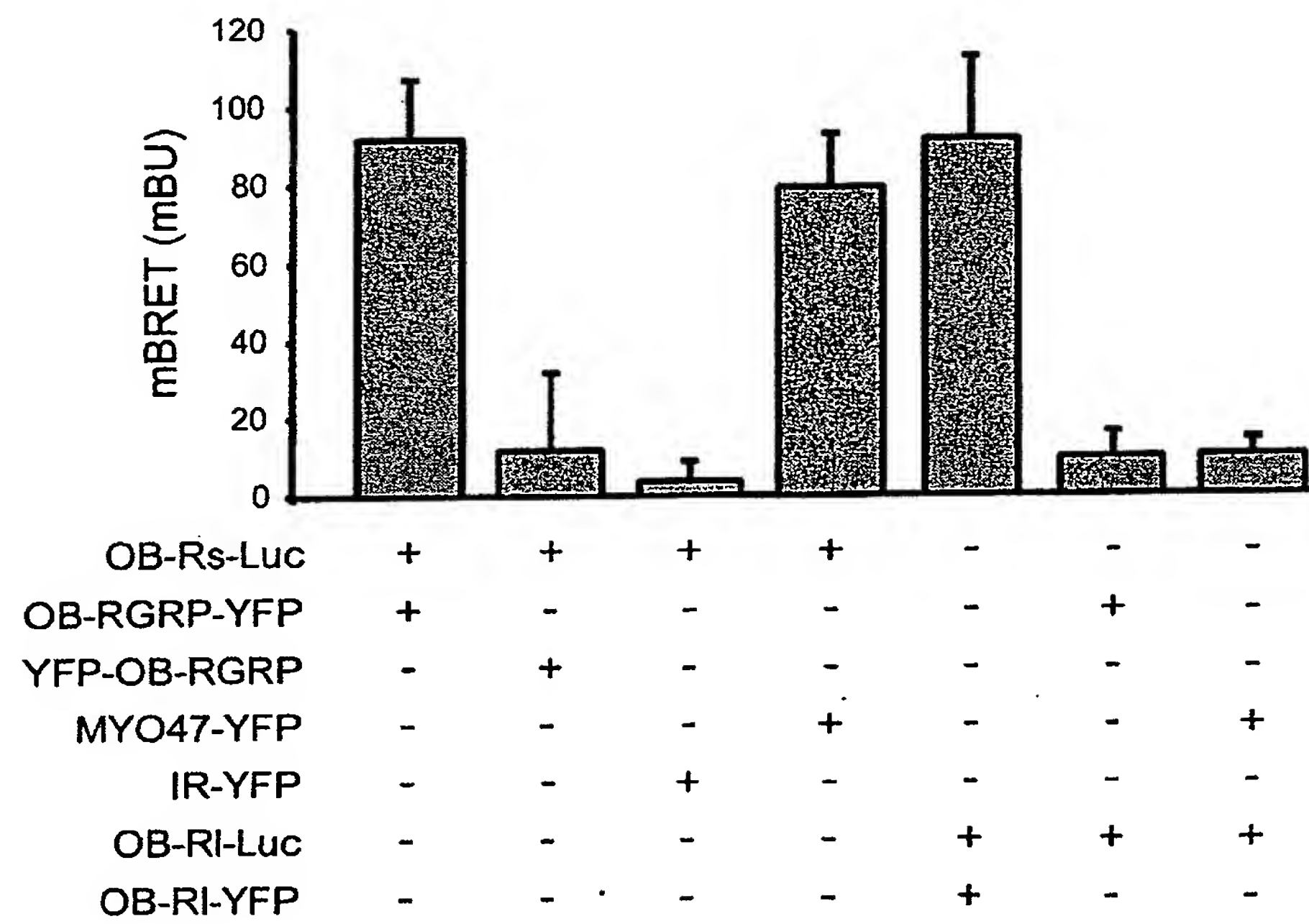
**Figure 7**

Figure 8a

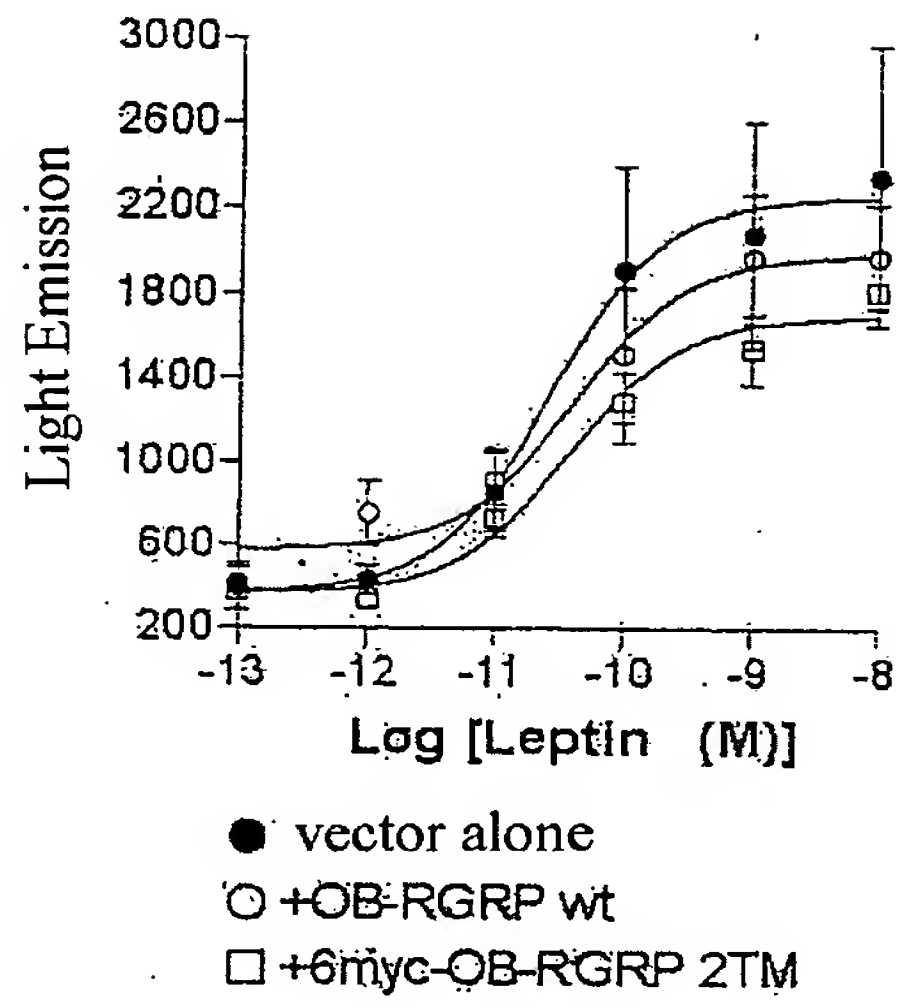
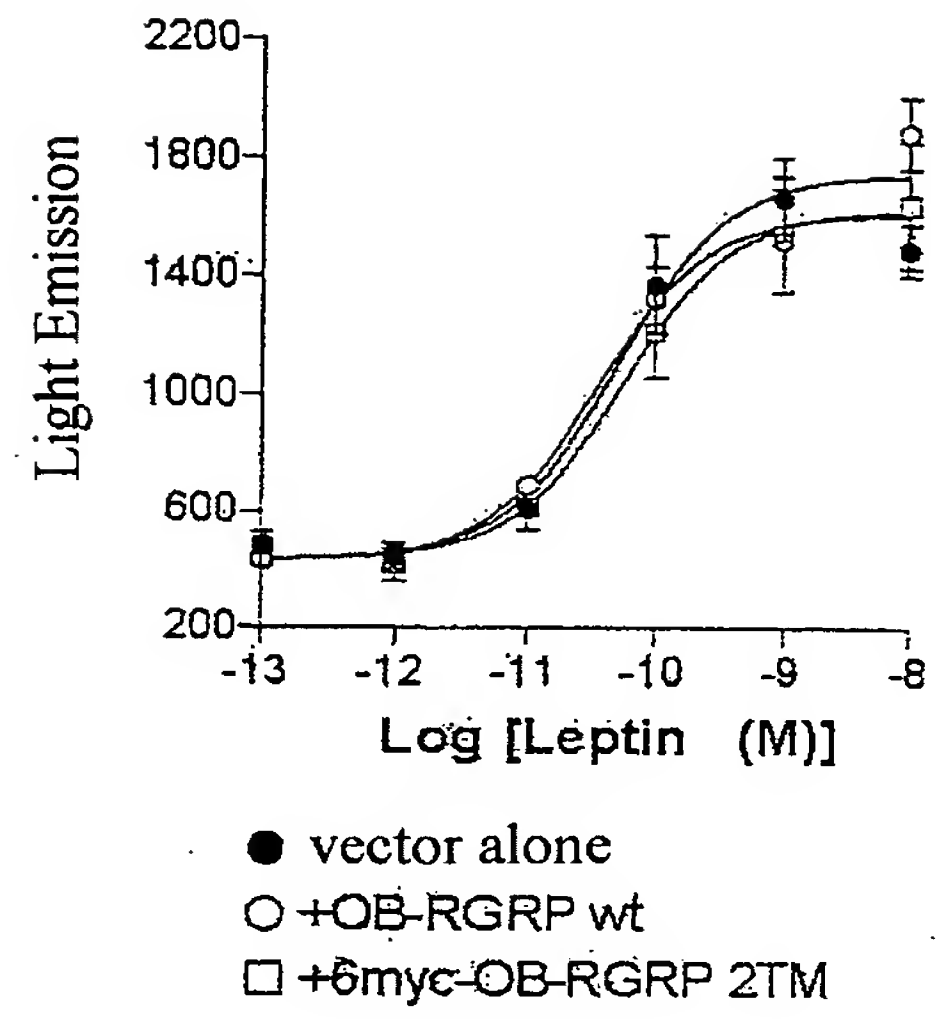


Figure 8b





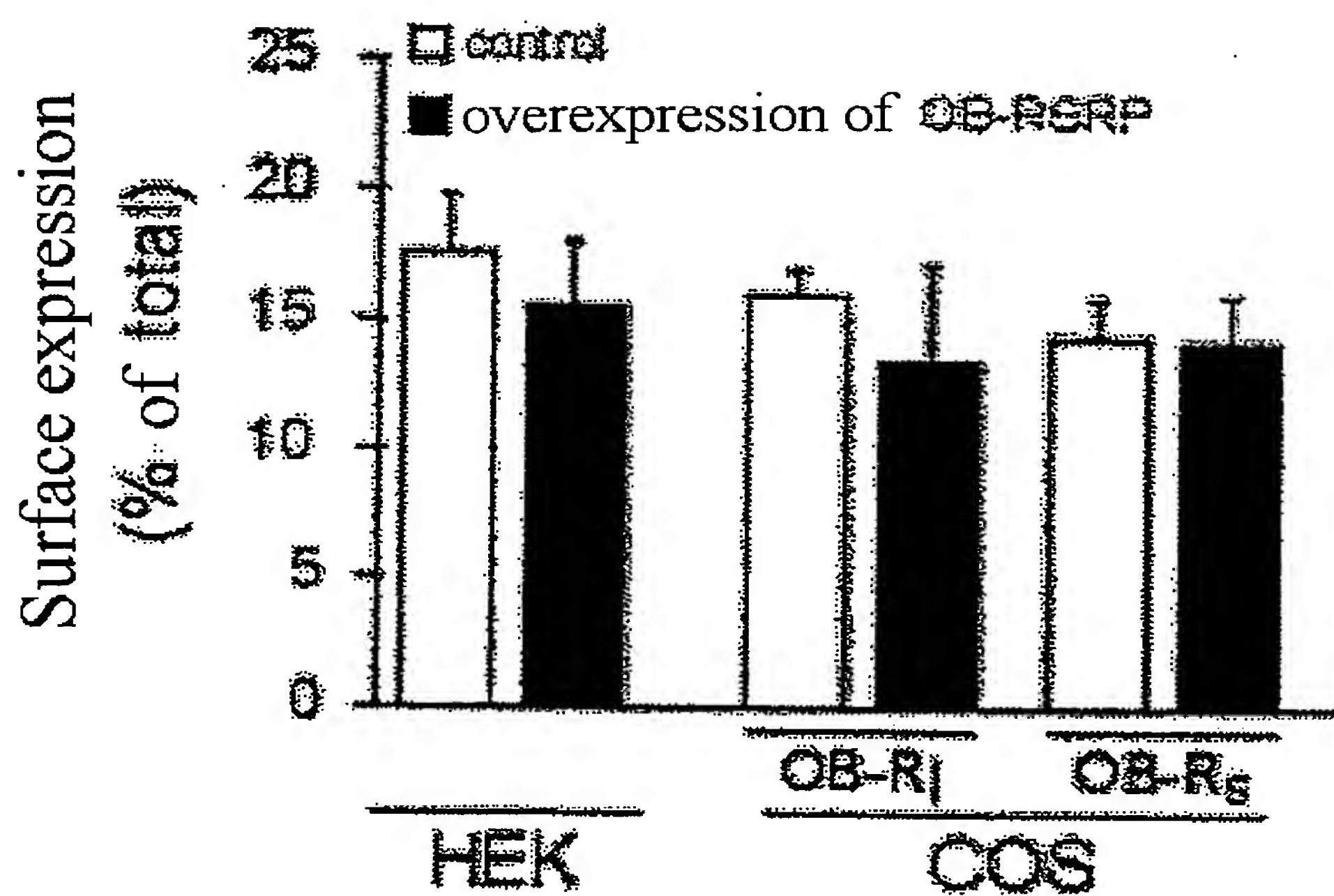
**Figure 9**

Figure 10a

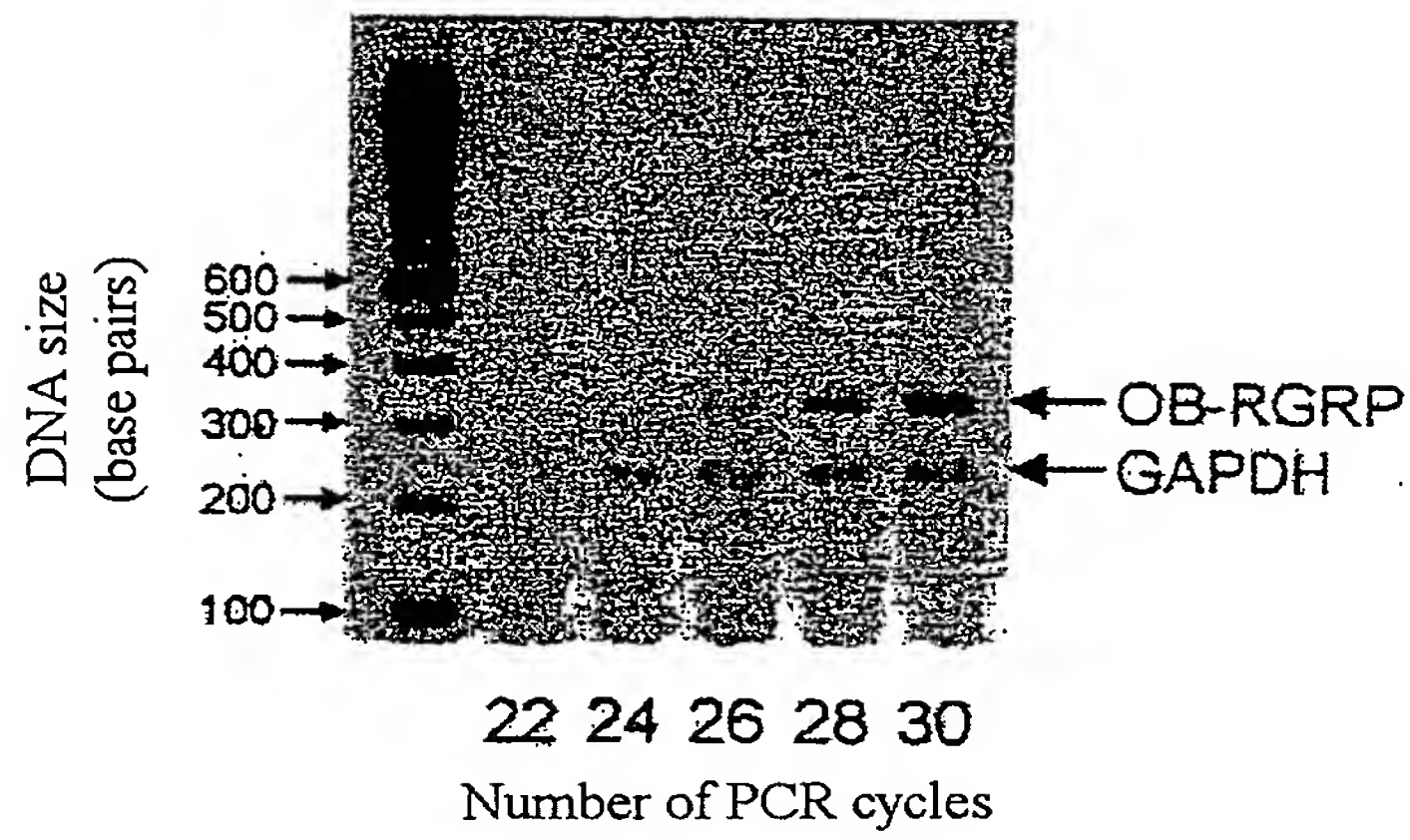


Figure 10b

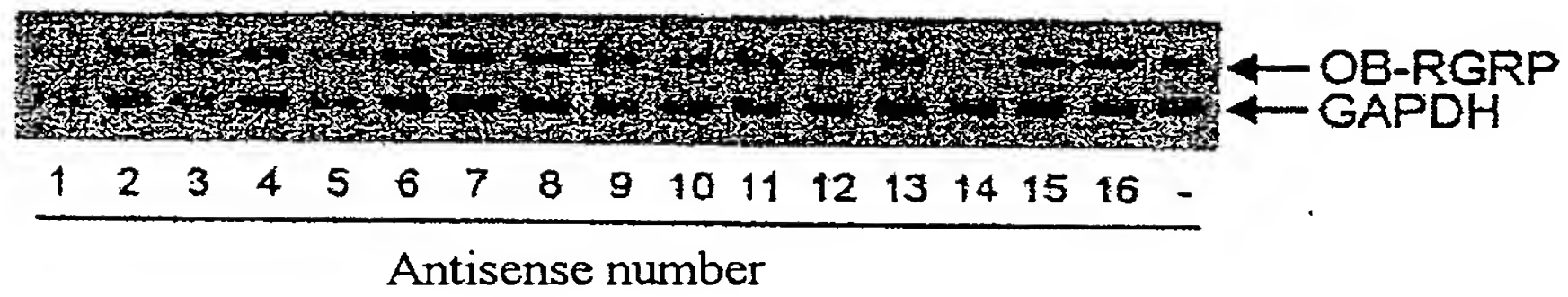
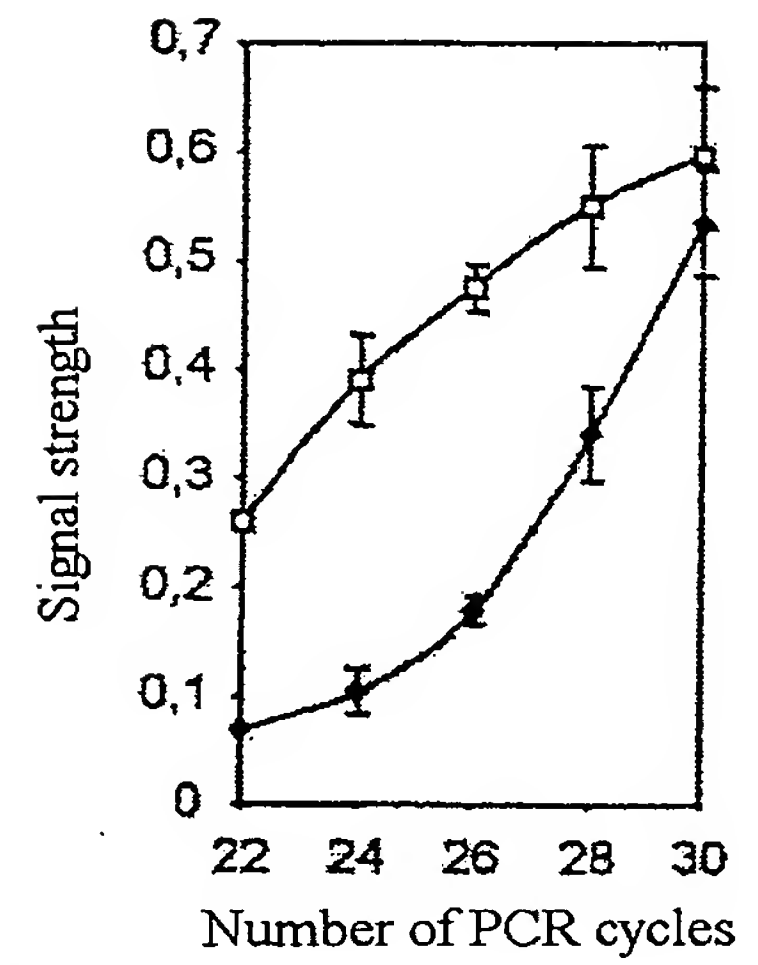


Figure 10c

FIGURE 11A

5' - gugccugucggggaacuggcTT -3'  
 3' - TTcacggacagcccuugaccg -5'

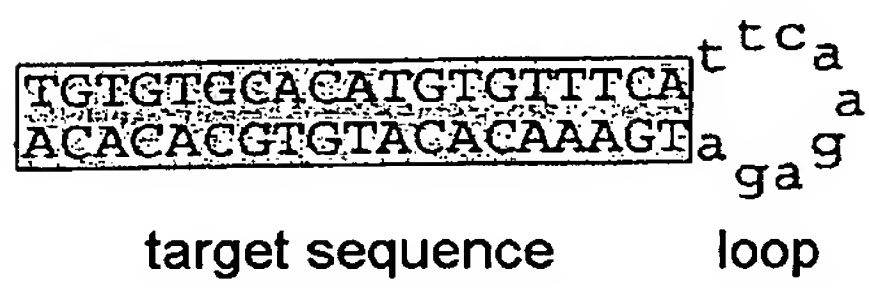


FIGURE 11C

FIGURE 11B

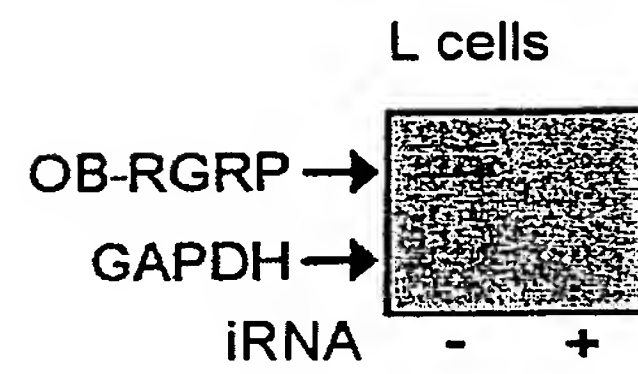
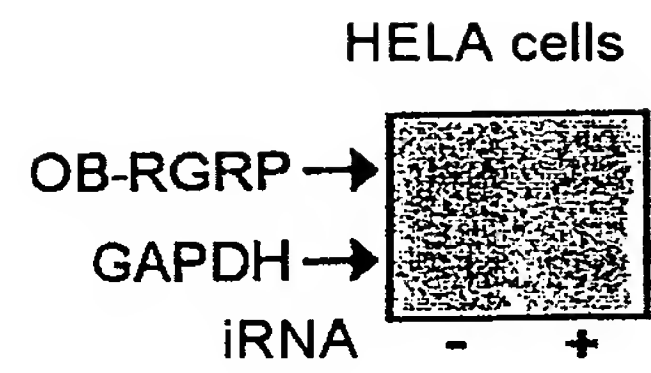
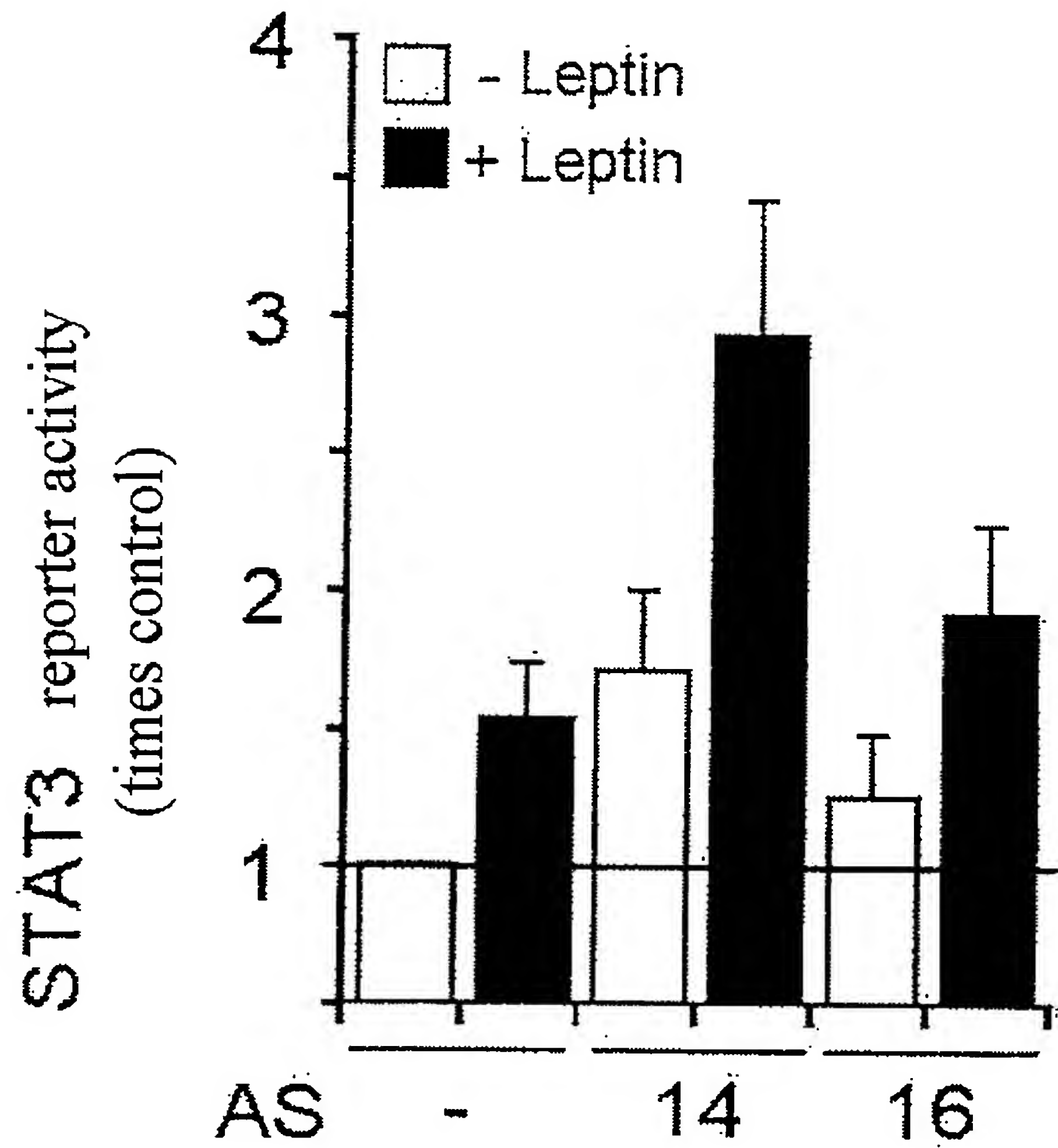


FIGURE 11D

**Figure 12**

**Figure 13**